

Appl. No.: 09/825,482

Patent

**Listing of Claims:**

1-49. (Canceled)

50. (Amended) A method for detecting whether at least one selected strain of human papilloma virus (HPV) is present in a sample, comprising:

providing a sample that may include nucleic acid from at least one selected strain of HPV and may include nucleic acid from at least one non-selected strain of HPV;

providing at least one primer substantially complementary to a region in both the nucleic acid from at least one selected strain of HPV and the nucleic acid from at least one non-selected strain of HPV;

providing at least one probe that is sufficiently complementary to a portion of the nucleic acid from at least one non-selected strain to block amplification of the nucleic acid from at least one non-selected strain, the at least one probe comprising PNA;

exposing the sample to said at least one primer and said at least one probe under conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified by a method selected from ligase chain reaction and rolling circle replication to produce an amplification product; and

detecting whether the amplification product is produced.

51. (Previously Presented) The method of claim 50, wherein at least one of said at least one selected strain comprises a pathogenic strain.

Appl. No.: 09/825,482

Patent

52. (Previously Presented) The method of claim 51, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.

53. (Previously Presented) The method of claim 50, wherein at least one of said at least one probe is a hybrid further comprising a nucleic acid other than PNA.

54. (Previously Presented) The method of claim 50, wherein at least one of said at least one probe comprises at least 8 bases.

55. (Cancelled)

56. (Cancelled)

57. (Previously Presented) The method of claim 50, wherein the conditions comprise conducting a ligase chain reaction.

58. (Previously Presented) The method of claim 50, wherein the conditions comprise conducting a rolling circle replication.

59. (Previously Presented) The method of claim 50, wherein at least one of said at least one primer is substantially complementary to a region of the HPV genome selected from L1, L2, E1, E6, and E7.

Appl. No.: 09/825,482

Patent

60. (Previously Presented) The method of claim 59, wherein said region of the HPV genome is L1.

61. (Previously Presented) The method of claim 59, wherein said region of the HPV genome is E6.

62. (Previously Presented) The method of claim 50, wherein said at least one non-selected strain comprises a plurality of low-risk HPV strains.

63. (Previously Presented) The method of claim 50, wherein said at least one non-selected strain comprises at least one strain selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

64. (Previously Presented) The method of claim 50, wherein said at least one selected strain comprises a plurality of high-risk HPV strains.

65. (Previously Presented) The method of claim 50, wherein said at least one selected strain comprises at least one strain selected from the group consisting of HPV strains 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

66. (Amended) The method of claim 50, wherein said at least one primer comprises a primer selected from MY09 (SEQ. ID. NO. 10) and MY11 (SEQ. ID. NO. 11).

Appl. No.: 09/825,482

Patent

67. (Amended) The method of claim 50, wherein said at least one probe comprises at least one probe selected from SEQ. ID. NO. 1, SEQ. ID. NO. 2, SEQ. ID. NO. 3, SEQ. ID. NO. 4, SEQ. ID. NO. 5, SEQ. ID. NO. 6 and, SEQ. ID. NO. 7, and SEQ. ID. NO. 8.

68. (Previously Presented) The method of claim 67, wherein said at least one probe comprises SEQ. ID. NO. 6.

69. (Previously Presented) The method of claim 67, wherein said at least one probe comprises SEQ. ID. NO. 7.

70. (Previously Presented) The method of claim 50, wherein said sample is a cervical scraping.

71. (Previously Presented) The method of claim 50, wherein detecting whether said amplification product is produced comprises in-gel electrophoresis and staining with ethidium bromide.

72. (Previously Presented) The method of claim 50, wherein a plurality of probes are provided, wherein each of said plurality is sufficiently complementary to a portion of the nucleic acid from a different non-selected strain.

Appl. No.: 09/825,482

Patent

73. (Previously Presented) The method of claim 50, wherein at least one of said at least one probe is substantially complementary to a portion of nucleic acid that is adjacent to the region of nucleic acid to which at least one of said at least one primer is substantially complementary.

74. (Previously Presented) A method for detecting whether at least one selected strain of human papilloma virus (HPV) is present in a sample, comprising:

providing a sample that may include nucleic acid from at least one selected strain of HPV and may include nucleic acid from at least one non-selected strain of HPV;

providing at least one primer substantially complementary to a region in both the nucleic acid from at least one selected strain of HPV and the nucleic acid from at least one non-selected strain of HPV;

providing at least one probe that is sufficiently complementary to a portion of the nucleic acid from at least one non-selected strain to block amplification of the nucleic acid from at least one non-selected strain, the at least one probe comprising PNA selected from the group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7;

exposing the sample to said at least one primer and said at least one probe under conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified to produce an amplification product; and

detecting whether the amplification product is produced.

75. (New) The method of claim 50 or 74, wherein said at least one primer comprises SEQ. ID. NO. 9.

Appl. No.: 09/825,482

Patent

76. (New) The method of claim 50 or 74, further comprising capturing said at least one selected strain onto a solid support.

77. (New) The method of claim 76, wherein said capturing comprises using an Alu oligonucleotide on said solid support to capture said at least one selected strain by hybridization.

78. (New) The method of claim 50 or 74, wherein at least one of said at least one probe is a molecular beacon.

79. (New) The method of claim 74, wherein at least one of said at least one selected strain comprises a pathogenic strain.

80. (New) The method of claim 79, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.

81. (New) The method of claim 74, wherein at least one of said at least one probe is a hybrid further comprising a nucleic acid other than PNA.

82. (New) The method of claim 74, wherein the conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified comprise conducting a reaction selected from the group consisting of a polymerase chain reaction, a ligase chain reaction, a rolling circle replication, a branched chain amplification, a nucleic acid based

Appl. No.: 09/825,482

Patent

sequence amplification (NASBA), a Cleavase Fragment Length Polymorphism, ICAN, and RAM.

83. (New) The method of claim 74, wherein the conditions comprise conducting a polymerase chain reaction, and said at least one primer comprises a primer pair suitable for amplifying said at least a part of said region.

84. (New) The method of claim 82, wherein the conditions comprise conducting a ligase chain reaction.

85. (New) The method of claim 82, wherein the conditions comprise conducting a rolling circle replication.

86. (New) The method of claim 74, wherein said at least one non-selected strain comprises a plurality of low-risk HPV strains.

87. (New) The method of claim 74, wherein said at least one non-selected strain comprises at least one strain selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

88. (New) The method of claim 74, wherein said at least one selected strain comprises a plurality of high-risk HPV strains.

Appl. No.: 09/825,482

Patent

89. (New) The method of claim 74, wherein said at least one selected strain comprises at least one strain selected from the group consisting of HPV strains 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

90. (New) The method of claim 74, wherein said at least one primer comprises a primer selected from MY09 (SEQ. ID. NO. 10) and MY11 (SEQ. ID. NO. 11).

91. (New) The method of claim 74, wherein said at least one probe comprises SEQ. ID. NO. 6.

92. (New) The method of claim 74, wherein said at least one probe comprises SEQ. ID. NO. 7.

93. (New) The method of claim 74, wherein said sample is a cervical scraping.

94. (New) The method of claim 74, wherein detecting whether said amplification product is produced comprises in-gel electrophoresis and staining with ethidium bromide.

95. (New) The method of claim 74, wherein a plurality of probes are provided, wherein each of said plurality is sufficiently complementary to a portion of the nucleic acid from a different non-selected strain.



**Appl. No.: 09/825,482****Patent**

96. (New) The method of claim 74, wherein at least one of said at least one probe is substantially complementary to a portion of nucleic acid that is adjacent to the region of nucleic acid to which at least one of said at least one primer is substantially complementary.